

WHAT IS CLAIMED IS:

1. A method of nucleic acid sequencing comprising the steps:

5 (a) amplifying a nucleic acid sample to produce an amplified DNA product;

(b) extending a sequencing primer bound to the DNA product in the presence of terminating nucleotide analogs to
10 produce a collection of labeled nucleic acid products;

(c) detecting a total amount of label present in the collection to produce a measurement; and

(d) combining a plurality of measurements to determine
15 DNA sequence information about the sample.

2. A method as described in Claim 1 wherein each measurement of a label corresponds to an amount of terminating nucleotide.

3. A method as described in Claim 1 wherein the DNA sequence information corresponds to a length of the DNA sequence.

4. A method as described in Claim 1 wherein the DNA sequence
25 information corresponds to a plurality of bases in the DNA sequence.

5. A method as described in Claim 1, wherein after the combining
30 step, the DNA sequence information is used for human identification.

6. A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used for diagnostic testing.

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7. A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used for genetic localization or gene discovery.

5 8. A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used for criminal justice applications.

10 9. A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used in conjunction with a DNA database of genetic polymorphisms.

10. A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used for cancer assessment.

11. A system for nucleic acid sequencing comprising:

(a) a means for amplifying a nucleic acid sample to produce an amplified nucleic acid product;

(b) a means for extending a sequencing primer bound to the DNA product in the presence of terminating nucleotide analogs to produce a collection of labeled nucleic acid products, said extending means in connection with the amplified product;

(c) a means for detecting a total amount of label present in the collection to produce a measurement, said detecting means in connection with the collection; and

(d) a means for combining a plurality of measurements to determine DNA sequence information about the sample, said combining means in connection with the measurement.

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16. A method as described in Claim 15 wherein the incomplete sequence information describes a genetic polymorphism.